

Genome Sequence of *Microbacterium testaceum* StLB037, an *N*-Acylhomoserine Lactone-Degrading Bacterium Isolated from Potato Leaves[▽]

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***Microbacterium testaceum* is an endophytic Gram-positive bacterium that resides within plant hosts. *M. testaceum* StLB037 was isolated from potato leaves and shows *N*-acylhomoserine lactone-degrading activity. Here, we present the 3.98-Mb complete genome sequence of StLB037, with an average GC content of 70.28%.**

The genus *Microbacterium* belongs to the class of high-GC-content *Actinobacteria*. *Microbacterium testaceum* is an endophytic bacterium that resides within plant hosts without causing disease symptoms (12). In many Gram-negative bacterial species, *N*-acylhomoserine lactone (AHL) has been identified as a signal compound involved in the quorum-sensing system (2). Many Gram-negative plant pathogens produce AHLs and regulate their virulence by AHL-mediated quorum sensing (10). We have reported the isolation of AHL-degrading *M. testaceum* strains from the leaf surface of the potato (6). We also cloned the *aiiM* gene from the genomic library of StLB037, which has AHL-lactonase activity and shows high homology with the α/β hydrolase fold family from *Actinobacteria* (11). To our knowledge, the complete genome sequence of the genus *Microbacterium* has not been deposited in the DDBJ/EMBL/GenBank databases at this point in time. In this work, we determined the genome sequence of *M. testaceum* StLB037.

Single- and paired-end whole-genome shotgun sequencing of StLB037 was performed using Roche genome sequencer FLX Titanium pyrosequencing technology (5) provided by Operon Biotechnologies (Tokyo, Japan). We produced 584,678 reads, with an average read length of 287 bases. The total number of sequenced bases is 167,947,725, representing a sequencing depth of 42 \times . With the use of Celera Assembler version 5.3, these reads were assembled into one large scaffold including 29 large contigs (>1,000 bp). Gap closure was attempted using gap-spanning clones and PCR products. Prediction of putative coding sequences and gene annotation were done using the Microbial Genome Annotation Pipeline (<http://migap.lifesciencedb.jp/>). Briefly, protein-coding sequences (CDSs) were predicted by the

combined use of MetaGeneAnnotator (7), RNAmmer (3), tRNAScan (4), and BLAST (1).

The complete genomic information for *M. testaceum* StLB037 is contained on a single circular chromosome of 3,982,034 bp with an average GC content of 70.28%. The genome contains 3,676 protein-coding genes, two rRNA operons, and 45 tRNA genes.

The *aiiM* gene, which has been identified from the genomic library of StLB037, was found as a single copy in the complete genome. Many AHL-degrading genes have been cloned and characterized from various bacterial species (8). We searched for the homologs of the reported AHL-degrading genes in the complete genome of StLB037. As a result, one predicted CDS (MTES_1124), which encoded 309 amino acids, showed 26.3% identity to the reported AHL-degrading enzyme, QsdA (9). QsdA is a phosphotriesterase-like AHL lactonase from *Rhodococcus erythropolis* W2, which belongs to the class of *Actinobacteria* as well as *M. testaceum*.

In summary, the AHL-degrading activity of *M. testaceum* StLB037 is effective for protection against plant pathogens. Therefore, the complete genome sequence of *M. testaceum* StLB037 will contribute to the development of biocontrol agents which quench quorum sensing in plant pathogens.

Nucleotide sequence accession number. The complete genome sequence of *M. testaceum* StLB037 has been deposited in the DDBJ/EMBL/GenBank databases under accession no. AP012052.

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